



SEQUENCE LISTING

<110> Tang et al.

<120> METHODS AND MATERIALS RELATING TO NOVEL STEM CELL GROWTH  
FACTOR-LIKE POLYPEPTIDES AND POLYNUCLEOTIDES

<130> 28110/37260A

<140>

<141> 2001-06-28

<150> To be assigned

<151> 2001-04-05

<150> 60/266,614

<151> 2001-02-05

<150> 60/215,733

<151> 2000-06-28

<150> 09/757,562

<151> 2001-01-09

<150> 09/543,774

<151> 2000-04-05

<160> 48

<170> PatentIn version 3.0

<210> 1

<211> 301

<212> DNA

<213> Homo sapiens

<400> 1

gcacgagacg agggaaaaaa ggaagggaga ggaaaagaaa aaaacctaataaaggagaaa	60
gtaaagaagc aatacctgac agcaaaagtc tggaatccag caaagaaatc ccagagcaac	120
gagaaaacaa acagcagcag aagaagcgaa aagtccaaga taaacagaaa tcggtatcag	180
tcagcactgt aactagagg gttccatgag attattgtag actcatgatg ctgctatctc	240
aaccagatgc ccaggacagg tgctctagcc attaggacca caaatggaca tgtcagttat	300
t	301

<210> 2

<211> 392

<212> DNA

<213> Homo sapiens

a!

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<400> 2
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tttcaacaaa gattttctgca caaaatgtaa aagtggattt tacttacacc ttggaaagtg      120
ccttgacaat tgcccagaag ggttggaagc caacaacat actatggagt gtgtcagtat      180
tgtgcactgt gaggtcagtg aatggaatcc ttggagtcca tgcacgaaga agggaaaaaac      240
atgtggcttc aaaagaggga ctgaaacacg ggtccgagaa ataatacagc atccttcagc      300
aaagggtaac ctatgtcccc caacaaatga gacaagaaag tgtacagtgc aaaggaagaa      360
gtgtcagaag ggagaacgag gaaaataagg ag                                     392

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<210> 3
<211> 475
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature

<222> (1)..(475)
<223> n = A, T, G, or C

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<400> 3
gtnagtaccc ccagggattt cactgagngc ctggactgag gaccgcgcna anngcnngan      60
ccacgcgtnc gcccacgcgt ccggagagga aaagaaaaaa acctaattta ggagaaagta      120
aagaagcaat acctgacagc ggaagtctgg aatggagcaa agaaatccca gagcaacgag      180
aaaacaaaca gcagcagaag aagcgaaaag tccaagataa acagaaatcg gtatcagtca      240
gcactgtaca ctagagggtt ccatgagatt attgtagact catgatgctg ctatctcaac      300
cagatgcccc ggacaggtgc tctagccatt aggaccacaa atggacatgt cagttattgc      360
tctgtctaaa caacattccc agtagttgct atattcttca tacaagcata gttaacaaca      420
aagagccaaa agatcaaaga agggatactt tcagatgggt gtcttgtgtg cttn          475

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<210> 4
<211> 473
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature

<222> (1)..(473)
<223> n = A, T, G, or C

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<400> 4
tgggcannnn aaanttttga nattcgatcc gcgctgcagg aattcggcac gagacgagga      60

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aaaaaaggaa gggagaggaa aagaaaaaaa cctaataaag gagaaagtaa agaagcaata 120
cctgacagca aaagtctgga atccagcaga gaaatcccag agcaacgaga aaacaaacag 180
cagcagaaga agcgaaaagt ccaagataaa cagaaatcgg tatcagtcag cactgtacac 240
tagaggggttc catgagatta ttgtagactc atgatgctgc tatctcaacc agatgcccag 300
gacagggtgct ctagccatta ggaccacaaa tggacatgct agttattgct ctgtctaaac 360
aacattccca gtagttgcta tattcttcat acaagcatag ttaacaacaa agagccaaaa 420
gatcaaagaa gggatacttt cagatgggtg tcttgtgtgc ttctctgcat ttt 473

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<210> 5
<211> 462
<212> DNA
<213> Homo sapiens

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<220>
<221> misc_feature
<222> (1)..(462)
<223> n = A, T, G, or C

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<400> 5
tgggagannn ntttgaaact gagatcgtcg canacnncac nangaataaa aggaagggag 60
agggaaagaa aaaaacctaa taaaggagaa agtaaagaat caatttctga cagcaaaagt 120
ctggaatcca tcaaagaaat cccatatcaa cgagaaaaca gacagcagca caaaaagcga 180
aaagtccaag ataaacagaa atcggatatca gtcagcactg tacactagag ggttccatga 240
gattattgta gactcatgat gctgctatct caaccagatg cccaggacag gtgctctatc 300
cattacgacc acaaattggac atgtcagtta ttgctctgtc taaacaacat tcccagtagt 360
tgctatatte ttcatacaag catagttaac acaaagagc caaaagatca aagaagggat 420
actttcagat ggttgtcttg tgtgcttctc tgcattttta aa 462

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<210> 6
<211> 384
<212> DNA
<213> Homo sapiens

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<400> 6
aataatgtgt acaaaatgca aagctgactg tgatacctgt ttcaacaaaa atttctgcac 60
aaaatgtaaa agtggatttt acttacacct tggaaagtgc cttgacaatt gccagaagg 120
gttggaagcc aacaaccata ctatggagtg tgtcagtatt gtgcactgtg aggtcagtga 180
atggaatcct tggagtccat gcacgaagaa gggaaaaaca tgtggcttca aaagagggac 240

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tgaaacacgg gtccgagaaa taatacagca tccttcagca aagggttaacc tatgtccccc 300  
aacaaatgag acaagaaaagt gtacagtgc aaggaagaag tgtcagaagg gagaacgagg 360  
aaaaaaagga agggagagga aaag 384

<210> 7  
<211> 390  
<212> DNA  
<213> Homo sapiens  
<220>  
<221> misc\_feature  
<222> (1)..(390)  
<223> n = A, T, G, or C

<400> 7  
cgttgctctg ggatttcttt gctggattcc agacttttgc tgtcaggat tgcttcttta 60  
ctttctcctt tattagggtt ttttcttttc ctctcccttc ctttttttcc tcgttctccc 120  
ttctgacact tcttcctttg cactgtacac tttcttgtct catttggttg gggacatagg 180  
ttaccctttg ctgaaggatg ctgtattatt tctcggacce gtgtttcagt ccctcttttg 240  
aagccacatg tttttccctt ctctgtgcat ggactccaag gattccattc actgacctca 300  
cagtgcacaa tactgacaca ctccatagta tgggtgttgg cttccaaccc ttctgggcaa 360  
ttgtcaaggc actttccaag gtgtaagtan 390

<210> 8  
<211> 1345  
<212> DNA  
<213> Homo sapiens  
<220>  
<221> misc\_feature  
<222> (321)..(1235)  
<223> similar to gi4519541 in the genpept database release 114, Run with FASTXY3.3t00, default parameter

<400> 8  
gcggccgccc cggcggctcc tggaaccccg gttcgcggcg atgccagcca cccagcgaa 60  
gcgcgcgcag ttcagtgcct ggataatttg aaagtacaat agttggtttc cctgtccacc 120  
cgccccactt cgcttgccat cacagcacgc ctatcggatg tgagaggaga agtcccgtg 180  
ctcgggcact gtctatatac gcctaacacc tacatatatt ttaaaaacat taaatataat 240  
taacaatcaa aagaaagagg agaaaggaag ggaagcatta ctgggttact atgcacttgc 300  
gactgatttc ttggcttttt atcattttga actttatgga atacatcggc agccaaaacg 360

cctccccggg	aaggcgccag	cgaagaatgc	atcctaacgt	tagtcaaggc	tgccaaggag	420
gctgtgcaac	atgctcagat	tacaatggat	gtttgtcatg	taagcccaga	ctatTTTTTg	480
ctctggaaag	aattggcatg	aagcagattg	gagtatgtct	catcttcatg	tccaagtgga	540
tattatggaa	ctcgatatcc	agatataaat	aatgtgtaca	aaatgcaaag	ctgactgtga	600
tacctgtttc	aacaaaaatt	tctgcacaaa	atgtaaaagt	ggattttact	tacaccttgg	660
aaagtgcctt	gacaattgcc	cagaagggtt	ggaagccaac	aaccatacta	tggagtgtgt	720
cagtattgtg	cactgtgagg	tcagtgaatg	gaatccttgg	agtccatgca	cgaagaaggg	780
aaaaacatgt	ggcttcaaaa	gagggactga	aacacgggtc	cgagaaataa	tacagcatcc	840
ttcagcaaag	ggtaacctat	gtcccccaac	aaatgagaca	agaaagtgtg	cagtgcaaag	900
gaagaagtgt	cagaaggagg	aacgaggaaa	aaaaggaagg	gagaggaaaa	gaaaaaaacc	960
taataaagga	gaaagtaaag	aagcaatacc	tgacagcaaa	agtctggaat	ccagcaaaga	1020
aatcccagag	caacgagaaa	acaaacagca	gcagaagaag	cgaaaagtcc	aagataaaca	1080
gaaatcggtg	tcagtcagca	ctgtacacta	gaggggtcca	tgagattatt	gtagactcat	1140
gatgctgcta	tctcaaccag	atgcccgagg	caggtgctct	agccattagg	accacaaatg	1200
gacatgtcag	ttattgctct	gtctaaacaa	cattcccagt	agttgctata	ttcttcatac	1260
aagcatagtt	aacaacaaag	agccaaaaga	tcaaagaagg	gatactttca	gatgggtgtc	1320
ttgtgtgctt	ctctgcattt	ttaaa				1345

<210> 9  
 <211> 1343  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (291)..(1109)

<400> 9	
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tggaaccccg	gttcgcggcg
atgccagcca	ccccagcgaa
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gccgccgag	ttcagtgtt
ggataatttg	aaagtacaat
agttggtttc	cctgtccacc
120	
cgccccactt	cgcttgccat
cacagcacgc	ctatcggatg
tgagaggaga	agtcccgtg
180	
ctcgggcact	gtctatatac
gcctaacacc	tacatatatt
ttaaaaacat	taaatataat
240	
taacaatcaa	aagaaagagg
agaaaggaag	ggaagcatta
ctgggttact	atg cac
296	Met His
	1

ttg cga ctg att tct tgg ctt ttt atc att ttg aac ttt atg gaa tac	344
Leu Arg Leu Ile Ser Trp Leu Phe Ile Ile Leu Asn Phe Met Glu Tyr	
5 10 15	

atc ggc agc caa aac gcc tcc cgg gga agg cgc cag cga aga atg cat	392
Ile Gly Ser Gln Asn Ala Ser Arg Gly Arg Arg Gln Arg Arg Met His	
20 25 30	
cct aac gtt agt caa ggc tgc caa gga ggc tgt gca aca tgc tca gat	440
Pro Asn Val Ser Gln Gly Cys Gln Gly Gly Cys Ala Thr Cys Ser Asp	
35 40 45 50	
tac aat gga tgt ttg tca tgt aag ccc aga cta ttt ttt gct ctg gaa	488
Tyr Asn Gly Cys Leu Ser Cys Lys Pro Arg Leu Phe Phe Ala Leu Glu	
55 60 65	
aga att ggc atg aag cag att gga gta tgt ctc tct tca tgt cca agt	536
Arg Ile Gly Met Lys Gln Ile Gly Val Cys Leu Ser Ser Cys Pro Ser	
70 75 80	
gga tat tat gga act cga tat cca gat ata aat aag tgt aca aaa tgc	584
Gly Tyr Tyr Gly Thr Arg Tyr Pro Asp Ile Asn Lys Cys Thr Lys Cys	
85 90 95	
aaa gct gac tgt gat acc tgt ttc aac aaa aat ttc tgc aca aaa tgt	632
Lys Ala Asp Cys Asp Thr Cys Phe Asn Lys Asn Phe Cys Thr Lys Cys	
100 105 110	
aaa agt gga ttt tac tta cac ctt gga aag tgc ctt gac aat tgc cca	680
Lys Ser Gly Phe Tyr Leu His Leu Gly Lys Cys Leu Asp Asn Cys Pro	
115 120 125 130	
gaa ggg ttg gaa gcc aac aac cat act atg gag tgt gtc agt att gtg	728
Glu Gly Leu Glu Ala Asn Asn His Thr Met Glu Cys Val Ser Ile Val	
135 140 145	
cac tgt gag gtc agt gaa tgg aat cct tgg agt cca tgc acg aag aag	776
His Cys Glu Val Ser Glu Trp Asn Pro Trp Ser Pro Cys Thr Lys Lys	
150 155 160	
gga aaa aca tgt ggc ttc aaa aga ggg act gaa aca cgg gtc cga gaa	824
Gly Lys Thr Cys Gly Phe Lys Arg Gly Thr Glu Thr Arg Val Arg Glu	
165 170 175	
ata ata cag cat cct tca gca aag ggt aac cta tgt ccc cca aca aat	872
Ile Ile Gln His Pro Ser Ala Lys Gly Asn Leu Cys Pro Pro Thr Asn	
180 185 190	
gag aca aga aag tgt aca gtg caa agg aag aag tgt cag aag gga gaa	920
Glu Thr Arg Lys Cys Thr Val Gln Arg Lys Lys Cys Gln Lys Gly Glu	
195 200 205 210	
cga gga aaa aaa gga agg gag agg aaa aga aaa aaa cct aat aaa gga	968
Arg Gly Lys Lys Gly Arg Glu Arg Lys Arg Lys Lys Pro Asn Lys Gly	
215 220 225	
gaa agt aaa gaa gca ata cct gac agc aaa agt ctg gaa tcc agc aaa	1016
Glu Ser Lys Glu Ala Ile Pro Asp Ser Lys Ser Leu Glu Ser Ser Lys	
230 235 240	
gaa atc cca gag caa cga gaa aac aaa cag cag cag aag aag cga aaa	1064
Glu Ile Pro Glu Gln Arg Glu Asn Lys Gln Gln Gln Lys Lys Arg Lys	
245 250 255	

gtc caa gat aaa cag aaa tcg gta tca gtc agc act gta cac tag 1109  
 Val Gln Asp Lys Gln Lys Ser Val Ser Val Ser Thr Val His  
 260 265 270

agggttccat gagattattg tagactcatg atgctgctat ctcaaccaga tgcccaggac 1169

agggtgctcta gccattagga ccacaaatgg acatgtcagt tattgctctg tctaaacaac 1229

attcccagta gttgctatat tcttcataca agcatagtta acaacaaaga gccaaaagat 1289

caaagaaggg atactttcag atgggtgtct tgtgtgcttc tctgcatttt taaa 1343

<210> 10  
 <211> 272  
 <212> PRT  
 <213> Homo sapiens

<400> 10

Met His Leu Arg Leu Ile Ser Trp Leu Phe Ile Ile Leu Asn Phe Met  
 1 5 10 15

Glu Tyr Ile Gly Ser Gln Asn Ala Ser Arg Gly Arg Arg Gln Arg Arg  
 20 25 30

Met His Pro Asn Val Ser Gln Gly Cys Gln Gly Gly Cys Ala Thr Cys  
 35 40 45

Ser Asp Tyr Asn Gly Cys Leu Ser Cys Lys Pro Arg Leu Phe Phe Ala  
 50 55 60

Leu Glu Arg Ile Gly Met Lys Gln Ile Gly Val Cys Leu Ser Ser Cys  
 65 70 75 80

Pro Ser Gly Tyr Tyr Gly Thr Arg Tyr Pro Asp Ile Asn Lys Cys Thr  
 85 90 95

Lys Cys Lys Ala Asp Cys Asp Thr Cys Phe Asn Lys Asn Phe Cys Thr  
 100 105 110

Lys Cys Lys Ser Gly Phe Tyr Leu His Leu Gly Lys Cys Leu Asp Asn  
 115 120 125

Cys Pro Glu Gly Leu Glu Ala Asn Asn His Thr Met Glu Cys Val Ser  
 130 135 140

Ile Val His Cys Glu Val Ser Glu Trp Asn Pro Trp Ser Pro Cys Thr  
 145 150 155 160

Lys Lys Gly Lys Thr Cys Gly Phe Lys Arg Gly Thr Glu Thr Arg Val  
165 170 175

Arg Glu Ile Ile Gln His Pro Ser Ala Lys Gly Asn Leu Cys Pro Pro  
180 185 190

Thr Asn Glu Thr Arg Lys Cys Thr Val Gln Arg Lys Lys Cys Gln Lys  
195 200 205

Gly Glu Arg Gly Lys Lys Gly Arg Glu Arg Lys Arg Lys Lys Pro Asn  
210 215 220

Lys Gly Glu Ser Lys Glu Ala Ile Pro Asp Ser Lys Ser Leu Glu Ser  
225 230 235 240

Ser Lys Glu Ile Pro Glu Gln Arg Glu Asn Lys Gln Gln Gln Lys Lys  
245 250 255

Arg Lys Val Gln Asp Lys Gln Lys Ser Val Ser Val Ser Thr Val His  
260 265 270

<210> 11

<211> 819

<212> DNA

<213> Homo sapiens

<400> 11

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tgccaaggag gctgtgcaac atgctcagat tacaatggat gtttgtcatg taagcccaga	180
ctattttttg ctctggaaag aattggcatg aagcagattg gagtatgtct ctcttcatgt	240
ccaagtggat attatggaac tcgatatcca gatataaata agtgtacaaa atgcaaagct	300
gactgtgata cctgtttcaa caaaaatttc tgcacaaaat gtaaaagtgg attttactta	360
caccttgga agtgccttga caattgcccc gaagggttgg aagccaacaa ccatactatg	420
gagtgtgtca gtattgtgca ctgtgaggtc agtgaatgga atccttggag tccatgcacg	480
aagaaggga aaacatgtgg cttcaaaaga gggactgaaa cacgggtccg agaaataata	540
cagcatcctt cagcaaagg taacctatgt cccccaacaa atgagacaag aaagtgtaca	600
gtgcaaagga agaagtgtca gaaggagaa cgaggaaaa aaggaaggga gaggaaaaga	660
aaaaaaccta ataaaggaga aagtaaagaa gcaatacctg acagcaaaag tctggaatcc	720



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agcaaagaaa tcccagagca acgagaaaac aaacagcagc agaagaagcg aaaagtccaa      780
gataaacaga aatcggtatc agtcagcact gtacactag                                819

<210> 12
<211> 822

<212> DNA

<213> Homo sapiens

<220>
<221> CDS

<222> (1)..(822)

<400> 12
atg ggt cac ttg cga ctg att tct tgg ctt ttt atc att ttg aac ttt      48
Met Gly His Leu Arg Leu Ile Ser Trp Leu Phe Ile Ile Leu Asn Phe
1      5      10      15

atg gaa tac atc ggc agc caa aac gcc tcc cgg gga agg cgc cag cga      96
Met Glu Tyr Ile Gly Ser Gln Asn Ala Ser Arg Gly Arg Arg Gln Arg
      20      25      30

aga atg cat cct aac gtt agt caa ggc tgc caa gga ggc tgt gca aca      144
Arg Met His Pro Asn Val Ser Gln Gly Cys Gln Gly Gly Cys Ala Thr
      35      40      45

tgc tca gat tac aat gga tgt ttg tca tgt aag ccc aga cta ttt ttt      192
Cys Ser Asp Tyr Asn Gly Cys Leu Ser Cys Lys Pro Arg Leu Phe Phe
      50      55      60

gct ctg gaa aga att ggc atg aag cag att gga gta tgt ctc tct tca      240
Ala Leu Glu Arg Ile Gly Met Lys Gln Ile Gly Val Cys Leu Ser Ser
65      70      75      80

tgt cca agt gga tat tat gga act cga tat cca gat ata aat aag tgt      288
Cys Pro Ser Gly Tyr Tyr Gly Thr Arg Tyr Pro Asp Ile Asn Lys Cys
      85      90      95

aca aaa tgc aaa gct gac tgt gat acc tgt ttc aac aaa aat ttc tgc      336
Thr Lys Cys Lys Ala Asp Cys Asp Thr Cys Phe Asn Lys Asn Phe Cys
      100      105      110

aca aaa tgt aaa agt gga ttt tac tta cac ctt gga aag tgc ctt gac      384
Thr Lys Cys Lys Ser Gly Phe Tyr Leu His Leu Gly Lys Cys Leu Asp
      115      120      125

aat tgc cca gaa ggg ttg gaa gcc aac aac cat act atg gag tgt gtc      432
Asn Cys Pro Glu Gly Leu Glu Ala Asn Asn His Thr Met Glu Cys Val
      130      135      140

agt att gtg cac tgt gag gtc agt gaa tgg aat cct tgg agt cca tgc      480
Ser Ile Val His Cys Glu Val Ser Glu Trp Asn Pro Trp Ser Pro Cys
145      150      155      160

acg aag aag gga aaa aca tgt ggc ttc aaa aga ggg act gaa aca cgg      528
Thr Lys Lys Gly Lys Thr Cys Gly Phe Lys Arg Gly Thr Glu Thr Arg
      165      170      175

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gtc cga gaa ata ata cag cat cct tca gca aag ggt aac cta tgt ccc	576
Val Arg Glu Ile Ile Gln His Pro Ser Ala Lys Gly Asn Leu Cys Pro	
180 185 190	
cca aca aat gag aca aga aag tgt aca gtg caa agg aag aag tgt cag	624
Pro Thr Asn Glu Thr Arg Lys Cys Thr Val Gln Arg Lys Lys Cys Gln	
195 200 205	
aag gga gaa cga gga aaa aaa gga agg gag agg aaa aga aaa aaa cct	672
Lys Gly Glu Arg Gly Lys Lys Gly Arg Glu Arg Lys Arg Lys Lys Pro	
210 215 220	
aat aaa gga gaa agt aaa gaa gca ata cct gac agc aaa agt ctg gaa	720
Asn Lys Gly Glu Ser Lys Glu Ala Ile Pro Asp Ser Lys Ser Leu Glu	
225 230 235 240	
tcc agc aaa gaa atc cca gag caa cga gaa aac aaa cag cag cag aag	768
Ser Ser Lys Glu Ile Pro Glu Gln Arg Glu Asn Lys Gln Gln Gln Lys	
245 250 255	
aag cga aaa gtc caa gat aaa cag aaa tcg gta tca gtc agc act gta	816
Lys Arg Lys Val Gln Asp Lys Gln Lys Ser Val Ser Val Ser Thr Val	
260 265 270	
cac tag	822
His	

<210> 13  
 <211> 273  
 <212> PRT  
 <213> Homo sapiens

<400> 13

Met Gly His Leu Arg Leu Ile Ser Trp Leu Phe Ile Ile Leu Asn Phe	
1 5 10 15	
Met Glu Tyr Ile Gly Ser Gln Asn Ala Ser Arg Gly Arg Arg Gln Arg	
20 25 30	
Arg Met His Pro Asn Val Ser Gln Gly Cys Gln Gly Gly Cys Ala Thr	
35 40 45	
Cys Ser Asp Tyr Asn Gly Cys Leu Ser Cys Lys Pro Arg Leu Phe Phe	
50 55 60	
Ala Leu Glu Arg Ile Gly Met Lys Gln Ile Gly Val Cys Leu Ser Ser	
65 70 75 80	
Cys Pro Ser Gly Tyr Tyr Gly Thr Arg Tyr Pro Asp Ile Asn Lys Cys	
85 90 95	

Thr Lys Cys Lys Ala Asp Cys Asp Thr Cys Phe Asn Lys Asn Phe Cys  
 100 105 110

Thr Lys Cys Lys Ser Gly Phe Tyr Leu His Leu Gly Lys Cys Leu Asp  
 115 120 125

Asn Cys Pro Glu Gly Leu Glu Ala Asn Asn His Thr Met Glu Cys Val  
 130 135 140

Ser Ile Val His Cys Glu Val Ser Glu Trp Asn Pro Trp Ser Pro Cys  
 145 150 155 160

Thr Lys Lys Gly Lys Thr Cys Gly Phe Lys Arg Gly Thr Glu Thr Arg  
 165 170 175

Val Arg Glu Ile Ile Gln His Pro Ser Ala Lys Gly Asn Leu Cys Pro  
 180 185 190

Pro Thr Asn Glu Thr Arg Lys Cys Thr Val Gln Arg Lys Lys Cys Gln  
 195 200 205

Lys Gly Glu Arg Gly Lys Lys Gly Arg Glu Arg Lys Arg Lys Lys Pro  
 210 215 220

Asn Lys Gly Glu Ser Lys Glu Ala Ile Pro Asp Ser Lys Ser Leu Glu  
 225 230 235 240

Ser Ser Lys Glu Ile Pro Glu Gln Arg Glu Asn Lys Gln Gln Gln Lys  
 245 250 255

Lys Arg Lys Val Gln Asp Lys Gln Lys Ser Val Ser Val Ser Thr Val  
 260 265 270

His

<210> 14  
 <211> 160

<212> PRT  
 <213> Homo sapiens

<400> 14

Cys Thr Lys Cys Lys Ala Asp Cys Asp Thr Cys Phe Asn Lys Asn Phe  
 1 5 10 15

Cys Thr Lys Cys Lys Ser Gly Phe Tyr Leu His Leu Gly Lys Cys Leu  
 20 25 30



Gly Thr Arg Tyr Pro Asp Ile Asn Lys Cys Thr Lys Cys Lys Ala Asp  
 65 70 75 80  
 Cys Asp Thr Cys Phe Asn Lys Asn Phe Cys Thr Lys Cys Lys Ser Gly  
 85 90 95  
 Phe Tyr Leu His Leu Gly Lys Cys Leu Asp Asn Cys Pro Glu Gly Leu  
 100 105 110  
 Glu Ala Asn Asn His Thr Met Glu Cys Val Ser Ile Val His Cys Glu  
 115 120 125  
 Val Ser Glu Trp Asn Pro Trp Ser Pro Cys Thr Lys Lys Gly Lys Thr  
 130 135 140  
 Cys Gly Phe Lys Arg Gly Thr Glu Thr Arg Val Arg Glu Ile Ile Gln  
 145 150 155 160  
 His Pro Ser Ala Lys Gly Asn Leu Cys Pro Pro Thr Asn Glu Thr Arg  
 165 170 175  
 Lys Cys Thr Val Gln Arg Lys Lys Cys Gln Lys Gly Glu Arg Gly Lys  
 180 185 190  
 Lys Gly Arg Glu Arg Lys Arg Lys Lys Pro Asn Lys Gly Glu Ser Lys  
 195 200 205  
 Glu Ala Ile Pro Asp Ser Lys Ser Leu Glu Ser Ser Lys Glu Ile Pro  
 210 215 220  
 Glu Gln Arg Glu Asn Lys Gln Gln Gln Lys Lys Arg Lys Val Gln Asp  
 225 230 235 240  
 Lys Gln Lys Ser Val Ser Val Ser Thr Val His  
 245 250

<210> 17  
 <211> 23  
 <212> PRT  
 <213> Homo sapiens

<400> 17

Ala Asp Cys Asp Thr Cys Phe Asn Lys Asn Phe Cys Thr Lys Cys Lys  
 1 5 10 15  
 Ser Gly Phe Tyr Leu His Leu  
 20

<210> 18  
 <211> 46  
 <212> PRT  
 <213> Homo sapiens

<400> 18

Ile Asn Lys Cys Thr Lys Cys Lys Ala Asp Cys Asp Thr Cys Phe Asn  
 1 5 10 15

Lys Asn Phe Cys Thr Lys Cys Lys Ser Gly Phe Tyr Leu His Leu Gly  
 20 25 30

Lys Cys Leu Asp Asn Cys Pro Glu Gly Leu Glu Ala Asn Asn  
 35 40 45

<210> 19

<211> 20

<212> PRT

<213> Homo sapiens

<400> 19

Met His Pro Asn Val Ser Gln Gly Cys Gln Gly Gly Cys Ala Thr Cys  
 1 5 10 15

Ser Asp Tyr Asn  
 20

<210> 20

<211> 37

<212> PRT

<213> Homo sapiens

<400> 20

Ile Val His Cys Glu Val Ser Glu Trp Asn Pro Trp Ser Pro Cys Thr  
 1 5 10 15

Lys Lys Gly Lys Thr Cys Gly Phe Lys Arg Gly Thr Glu Thr Arg Val  
 20 25 30

Arg Glu Ile Ile Gln  
 35

<210> 21

<211> 10

<212> PRT

<213> Homo sapiens

<400> 21

Lys Lys Gly Arg Glu Arg Lys Arg Lys Lys  
 1 5 10

<210> 22

<211> 42

<212> PRT

<213> Homo sapiens

<400> 22

Lys Cys Thr Val Gln Arg Lys Lys Cys Gln Lys Gly Glu Arg Gly Lys  
1 5 10 15

Lys Gly Arg Glu Arg Lys Arg Lys Lys Pro Asn Lys Gly Glu Ser Lys  
20 25 30

Glu Ala Ile Pro Asp Ser Lys Ser Leu Glu  
35 40

<210> 23

<211> 14

<212> PRT

<213> Homo sapiens

<400> 23

Thr Cys Phe Asn Lys Asn Phe Cys Thr Lys Cys Lys Ser Gly  
1 5 10

<210> 24

<211> 20

<212> PRT

<213> Homo sapiens

<400> 24

Cys Glu Val Ser Glu Trp Asn Pro Trp Ser Pro Cys Thr Lys Lys Gly  
1 5 10 15

Lys Thr Cys Gly  
20

<210> 25

<211> 229

<212> PRT

<213> Mus musculus

<400> 25

Val Gly Ser Arg Gly Ile Lys Gly Lys Arg Gln Arg Arg Ile Ser Ala  
1 5 10 15

Glu Gly Ser Gln Ala Cys Ala Lys Gly Cys Glu Leu Cys Ser Glu Val  
20 25 30

Asn Gly Cys Leu Lys Cys Ser Pro Lys Leu Phe Ile Leu Leu Glu Arg  
35 40 45

Asn Asp Ile Arg Gln Val Gly Val Cys Leu Pro Ser Cys Pro Pro Gly  
 50 55 60  
 Tyr Phe Asp Ala Arg Asn Pro Asp Met Asn Lys Cys Ile Lys Cys Lys  
 65 70 75 80  
 Ile Glu His Cys Glu Ala Cys Phe Ser His Asn Phe Cys Thr Lys Cys  
 85 90 95  
 Gln Glu Ala Leu Tyr Leu His Lys Gly Arg Cys Tyr Pro Ala Cys Pro  
 100 105 110  
 Glu Gly Ser Thr Ala Ala Asn Ser Thr Met Glu Cys Gly Ser Pro Ala  
 115 120 125  
 Gln Cys Glu Met Ser Glu Trp Ser Pro Trp Gly Pro Cys Ser Lys Lys  
 130 135 140  
 Arg Lys Leu Cys Gly Phe Arg Lys Gly Ser Glu Glu Arg Thr Arg Arg  
 145 150 155 160  
 Val Leu His Ala Pro Gly Gly Asp His Thr Thr Cys Ser Asp Thr Lys  
 165 170 175  
 Glu Thr Arg Lys Cys Thr Val Arg Arg Thr Pro Cys Pro Glu Gly Gln  
 180 185 190  
 Lys Arg Arg Lys Gly Gly Gln Gly Arg Arg Glu Asn Ala Asn Arg His  
 195 200 205  
 Pro Ala Arg Lys Asn Ser Lys Glu Pro Arg Ser Asn Ser Arg Arg His  
 210 215 220  
 Lys Gly Gln Gln Gln  
 225

<210> 26

<211> 265

<212> PRT

<213> Homo sapiens

<400> 26

Met His Leu Arg Leu Ile Ser Trp Leu Phe Ile Ile Leu Asn Phe Met  
 1 5 10 15  
 Glu Tyr Ile Gly Ser Gln Asn Ala Ser Arg Gly Arg Arg Gln Arg Arg  
 20 25 30  
 Met His Pro Asn Val Ser Gln Gly Cys Gln Gly Gly Cys Ala Thr Cys  
 35 40 45  
 Ser Asp Tyr Asn Gly Cys Leu Ser Cys Lys Pro Arg Leu Phe Phe Ala  
 50 55 60  
 Leu Glu Arg Ile Gly Met Lys Gln Ile Gly Val Cys Leu Ser Ser Cys  
 65 70 75 80



Pro Ser Gly Tyr Tyr Gly Thr Arg Tyr Pro Asp Ile Asn Lys Cys Thr  
                             85                            90                            95  
 Lys Cys Lys Ala Asp Cys Asp Thr Cys Phe Asn Lys Asn Phe Cys Thr  
                             100                            105                            110  
 Lys Cys Lys Ser Gly Phe Tyr Leu His Leu Gly Lys Cys Leu Asp Asn  
                             115                            120                            125  
 Cys Pro Glu Gly Leu Glu Ala Asn Asn His Thr Met Glu Cys Val Ser  
                             130                            135                            140  
 Ile Val His Cys Glu Val Ser Glu Trp Asn Pro Trp Ser Pro Cys Thr  
                             145                            150                            155                            160  
 Lys Lys Gly Lys Thr Cys Gly Phe Lys Arg Gly Thr Glu Thr Arg Val  
                             165                            170                            175  
 Arg Glu Ile Ile Gln His Pro Ser Ala Lys Gly Asn Leu Cys Pro Pro  
                             180                            185                            190  
 Thr Asn Glu Thr Arg Lys Cys Thr Val Gln Arg Lys Lys Cys Gln Lys  
                             195                            200                            205  
 Gly Glu Arg Gly Lys Lys Gly Arg Glu Arg Lys Arg Lys Lys Pro Asn  
                             210                            215                            220  
 Lys Gly Glu Ser Lys Glu Ala Ile Pro Asp Ser Lys Ser Leu Glu Ser  
                             225                            230                            235                            240  
 Ser Lys Glu Ile Pro Glu Gln Arg Glu Asn Lys Gln Gln Gln Lys Lys  
                             245                            250                            255  
 Arg Lys Val Gln Asp Lys Gln Lys Ser  
                             260                            265

<210> 27  
 <211> 8  
 <212> PRT  
 <213> Homo sapiens

<400> 27

Ser Val Ser Val Ser Thr Val His  
   1                            5

<210> 28  
 <211> 7  
 <212> PRT  
 <213> Homo sapiens

<400> 28

Val Ser Val Ser Thr Val His  
   1                            5

<210> 29  
 <211> 27  
 <212> PRT  
 <213> Homo sapiens  
 <400> 29

Gly	Ile	Glu	Val	Thr	Leu	Ala	Glu	Gly	Leu	Thr	Ser	Val	Ser	Gln	Arg
1				5				10						15	
Thr	Gln	Pro	Thr	Pro	Cys	Arg	Arg	Arg	Tyr	Leu					
			20					25							

<210> 30  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Description of Artificial Sequence: PCR primer  
 <400> 30

ctcgggaaga agcgcgccat ttgtgttggt 30

<210> 31  
 <211> 2384  
 <212> DNA  
 <213> Mus musculus

<220>  
 <221> CDS  
 <222> (511)..(1347)

<220>  
 <221> misc\_feature  
 <222> (2367)..(2367)  
 <223> n = A, T, G, or C  
 <400> 31

ggagcggctc ctgtcagaa cgccagaagc agctcgggtc tctccagcgc cccttgacca 60  
 tggtgcggt acccacggcg tccgcttccc tgcgctcccg gggtccttgc cacagccgca 120  
 gccgtgcag cctctgagcc ccaggggcca ctgctcgctt ggattccgcc cgcagccgcc 180  
 gctgctgtgc aaccgaggct aacctgcggc cagccaggag gctcctgcaa ccttcgctcg 240  
 cggcgatgac agccacccca gagcagccgg ctgtgttcgg acaatttgag aatgcaattg 300  
 ttggtttccc ggtccacccg tcccgcttcg cttgccatca cagcacgcct gttggatctc 360  
 agtggagaag tcccgctgct ctgggttttc tactcttcgt atagactcgc ctaacaccta 420  
 catacatatt tttcttttaa aaaaaacatt aaatataact aacagtgaaa agaaaaagga 480

gagaaaaaag ggaaacatta caggggttact atg cac ttg cga ctg att tct tgt 534  
Met His Leu Arg Leu Ile Ser Cys  
1 5

ttt ttt atc att ttg aac ttt atg gaa tac att ggc agc caa aac gcc 582  
Phe Phe Ile Ile Leu Asn Phe Met Glu Tyr Ile Gly Ser Gln Asn Ala  
10 15 20

tcc cga gga agg cgc cag cga aga atg cat cct aat gtc agt caa ggc 630  
Ser Arg Gly Arg Arg Gln Arg Arg Met His Pro Asn Val Ser Gln Gly  
25 30 35 40

tgc caa gga ggc tgt gca acg tgt tca gat tac aat ggc tgt ttg tca 678  
Cys Gln Gly Gly Cys Ala Thr Cys Ser Asp Tyr Asn Gly Cys Leu Ser  
45 50 55

tgt aag ccc aga ctg ttt ttt gtt ctg gaa agg att ggc atg aag cag 726  
Cys Lys Pro Arg Leu Phe Phe Val Leu Glu Arg Ile Gly Met Lys Gln  
60 65 70

ata gga gtg tgt ctc tct tcg tgt cca agt gga tat tac gga act cga 774  
Ile Gly Val Cys Leu Ser Ser Cys Pro Ser Gly Tyr Tyr Gly Thr Arg  
75 80 85

tat cca gat ata aat aaa tgt aca aaa tgc aaa gtt gac tgt gat acc 822  
Tyr Pro Asp Ile Asn Lys Cys Thr Lys Cys Lys Val Asp Cys Asp Thr  
90 95 100

tgt ttc aac aaa aat ttc tgc aca aag tgt aaa agt gga ttt tac tta 870  
Cys Phe Asn Lys Asn Phe Cys Thr Lys Cys Lys Ser Gly Phe Tyr Leu  
105 110 115 120

cac ctt gga aag tgc ctt gac agt tgc cca gaa ggg tta gaa gcc aac 918  
His Leu Gly Lys Cys Leu Asp Ser Cys Pro Glu Gly Leu Glu Ala Asn  
125 130 135

aat cat act atg gaa tgt gtc agt att gta cac tgt gag gcc agt gaa 966  
Asn His Thr Met Glu Cys Val Ser Ile Val His Cys Glu Ala Ser Glu  
140 145 150

tgg agt cca tgg agt cca tgt atg aag aaa gga aaa aca tgt ggc ttc 1014  
Trp Ser Pro Trp Ser Pro Cys Met Lys Lys Gly Lys Thr Cys Gly Phe  
155 160 165

aaa agg ggg act gaa aca cgg gtc cga gat ata cta cag cat cct tca 1062  
Lys Arg Gly Thr Glu Thr Arg Val Arg Asp Ile Leu Gln His Pro Ser  
170 175 180

gcc aag ggt aag ggt aac ctg tgc ccc cca acc agc gag aca aga act 1110  
Ala Lys Gly Lys Gly Asn Leu Cys Pro Pro Thr Ser Glu Thr Arg Thr  
185 190 195 200

tgt ata gta caa aga aag aag tgt tca aag gga gag cga gga aaa aag 1158  
Cys Ile Val Gln Arg Lys Lys Cys Ser Lys Gly Glu Arg Gly Lys Lys  
205 210 215

gga aga gag aga aaa cga aaa aaa ctg aat aaa gaa gaa aga aag gaa 1206  
Gly Arg Glu Arg Lys Arg Lys Lys Leu Asn Lys Glu Glu Arg Lys Glu  
220 225 230

aca agc tcc tcc tct gac agc aaa ggt ttg gag tcc agc att gag acc 1254  
 Thr Ser Ser Ser Ser Asp Ser Lys Gly Leu Glu Ser Ser Ile Glu Thr  
           235                                  240                                  245

cca gac cag cag gaa aac aaa gag agg cag cag cag cag aag aga aga 1302  
 Pro Asp Gln Gln Glu Asn Lys Glu Arg Gln Gln Gln Gln Lys Arg Arg  
           250                                  255                                  260

gcc cga gac aag caa cag aaa tcg gta tca gtc agc act gta cac 1347  
 Ala Arg Asp Lys Gln Lys Ser Val Ser Val Ser Thr Val His  
           265                                  270                                  275

tagaggggtcc tgcgagggtta ctgtagactc atgatgctgc tatctcaacc agatgtccag 1407

gacaggtggt ctagccatta gaaccacaaa tggacaacac atcagttacc actctgtcta 1467

aacaacattc ctaatagttg ctatattctt catacaaaca tagtaaacag caaagagcca 1527

aatgttcaaa gaagggatac tttcagatgg ttatcttatg tgcttctgtg tattttttaa 1587

agatgagaaa atttgtacat aattatcaat aagctataag atatcctcaa tgtaatgacg 1647

acagctggac aagaatcatc ttttctttat aaaaaaatta ttcttcgaat aattgtcttt 1707

aagaagcaaa aggtaattct gcaacttcaa aaatgcagtg tccctcaaaa ccaagatttg 1767

tcaggggaga gaatcatggc tccatgtaca ggggtggattt gtcccggaga actagtgaat 1827

gctcagaatt agggcctggc attttgaatc ctagagttaa tcatcacaga agcaagtgg 1887

ttaggattgc ttcggttgcc ctccctctgca agaaactgaa catgcataat agagttaa 1947

atattgtgtg gagttggaat aaggcaagct gtggaagaaa tcatagagct ggagaccatc 2007

ttgtgctttc cagaaccgtg aggggttttg gtcacctgga acagggctcc aatctatatt 2067

agcactgtgt ggttgatctt ccactactcc ttggtttata taagtctgta aacatgtacc 2127

tgtaaccttc ttccaaaagt aaaaccatac ttactagaag aaaattctaa ctttatggaa 2187

aacaaaagtg taagaagaat gtgacatggt tgcaaagttg agtggtttct ttctgaaatg 2247

aggggaaaac tattttatta cctgcctatg ggtccacctg gaactaaagg gatactactt 2307

tctaacaagg tgtatctagt aggagagaaa gccaccacaa taaatatatt tgттаatagn 2367

taaaaaaaaa aaaaaaa 2384

<210> 32  
 <211> 279  
 <212> PRT  
 <213> Mus musculus

<400> 32  
 Met His Leu Arg Leu Ile Ser Cys Phe Phe Ile Ile Leu Asn Phe Met  
           1                                  5                                  10                                  15

Glu Tyr Ile Gly Ser Gln Asn Ala Ser Arg Gly Arg Arg Gln Arg Arg  
           20                                  25                                  30

Met His Pro Asn Val Ser Gln Gly Cys Gln Gly Gly Cys Ala Thr Cys  
           35                          40                          45  
 Ser Asp Tyr Asn Gly Cys Leu Ser Cys Lys Pro Arg Leu Phe Phe Val  
           50                          55                          60  
 Leu Glu Arg Ile Gly Met Lys Gln Ile Gly Val Cys Leu Ser Ser Cys  
           65                          70                          75                          80  
 Pro Ser Gly Tyr Tyr Gly Thr Arg Tyr Pro Asp Ile Asn Lys Cys Thr  
                           85                          90                          95  
 Lys Cys Lys Val Asp Cys Asp Thr Cys Phe Asn Lys Asn Phe Cys Thr  
                           100                          105                          110  
 Lys Cys Lys Ser Gly Phe Tyr Leu His Leu Gly Lys Cys Leu Asp Ser  
           115                          120                          125  
 Cys Pro Glu Gly Leu Glu Ala Asn Asn His Thr Met Glu Cys Val Ser  
           130                          135                          140  
 Ile Val His Cys Glu Ala Ser Glu Trp Ser Pro Trp Ser Pro Cys Met  
           145                          150                          155                          160  
 Lys Lys Gly Lys Thr Cys Gly Phe Lys Arg Gly Thr Glu Thr Arg Val  
                           165                          170                          175  
 Arg Asp Ile Leu Gln His Pro Ser Ala Lys Gly Lys Gly Asn Leu Cys  
                           180                          185                          190  
 Pro Pro Thr Ser Glu Thr Arg Thr Cys Ile Val Gln Arg Lys Lys Cys  
           195                          200                          205  
 Ser Lys Gly Glu Arg Gly Lys Lys Gly Arg Glu Arg Lys Arg Lys Lys  
           210                          215                          220  
 Leu Asn Lys Glu Glu Arg Lys Glu Thr Ser Ser Ser Ser Asp Ser Lys  
           225                          230                          235                          240  
 Gly Leu Glu Ser Ser Ile Glu Thr Pro Asp Gln Gln Glu Asn Lys Glu  
                           245                          250                          255  
 Arg Gln Gln Gln Gln Lys Arg Arg Ala Arg Asp Lys Gln Gln Lys Ser  
                           260                          265                          270  
 Val Ser Val Ser Thr Val His  
           275

<210> 33

<211> 2101

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (259)..(1074)

<400> 33

tcgcggcgat gccagccacc ccagcgaagc cgccgcagtt cagtgccttg ataatttgaa 60

agtacaaatag ttgggtttccc tgtccacccg ccccacttcg cttgccatca cagcacgcct															120
atcgggatgtg agaggagaag tcccgtctgt cgggcactgt ctatatacgc ctaacaccta															180
catatatattt aaaaacatta aatataatta acaatcaaaa gaaagaggag aaaggaaggg															240
aagcattact ggggttact atg cac ttg cga ctg att tct tgg ctt ttt atc															291
Met His Leu Arg Leu Ile Ser Trp Leu Phe Ile															
1 5 10															
att ttg aac ttt atg gaa tac atc ggc agc caa aac gcc tcc cgg gga															339
Ile Leu Asn Phe Met Glu Tyr Ile Gly Ser Gln Asn Ala Ser Arg Gly															
15 20 25															
agg cgc cag cga aga atg cat cct aac gtt agt caa ggc tgc caa gga															387
Arg Arg Gln Arg Arg Met His Pro Asn Val Ser Gln Gly Cys Gln Gly															
30 35 40															
ggc tgt gca aca tgc tca gat tac aat gga tgt ttg tca tgt aag ccc															435
Gly Cys Ala Thr Cys Ser Asp Tyr Asn Gly Cys Leu Ser Cys Lys Pro															
45 50 55															
aga cta ttt ttt gct ctg gaa aga att ggc atg aag cag att gga gta															483
Arg Leu Phe Phe Ala Leu Glu Arg Ile Gly Met Lys Gln Ile Gly Val															
60 65 70 75															
tgt ctc tct tca tgt cca agt gga tat tat gga act cga tat cca gat															531
Cys Leu Ser Ser Cys Pro Ser Gly Tyr Tyr Gly Thr Arg Tyr Pro Asp															
80 85 90															
ata aat aag tgt aca aaa tgc aaa gct gac tgt gat acc tgt ttc aac															579
Ile Asn Lys Cys Thr Lys Cys Lys Ala Asp Cys Asp Thr Cys Phe Asn															
95 100 105															
aaa aat ttc tgc aca aaa tgt aaa agt gga ttt tac tta cac ctt gga															627
Lys Asn Phe Cys Thr Lys Cys Lys Ser Gly Phe Tyr Leu His Leu Gly															
110 115 120															
aag tgc ctt gac aat tgc cca gaa ggg ttg gaa gcc aac aac cat act															675
Lys Cys Leu Asp Asn Cys Pro Glu Gly Leu Glu Ala Asn Asn His Thr															
125 130 135															
atg gag tgt gtc agt att gtg cac tgt gag gtc agt gaa tgg aat cct															723
Met Glu Cys Val Ser Ile Val His Cys Glu Val Ser Glu Trp Asn Pro															
140 145 150 155															
tgg agt cca tgc acg aag aag gga aaa aca tgt ggc ttc aaa aga ggg															771
Trp Ser Pro Cys Thr Lys Lys Gly Lys Thr Cys Gly Phe Lys Arg Gly															
160 165 170															
act gaa aca cgg gtc cga gaa ata ata cag cat cct tca gca aag ggt															819
Thr Glu Thr Arg Val Arg Glu Ile Ile Gln His Pro Ser Ala Lys Gly															
175 180 185															
aac cta tgt ccc cca aca aat gag aca aga aag tgt aca gtg caa agg															867
Asn Leu Cys Pro Pro Thr Asn Glu Thr Arg Lys Cys Thr Val Gln Arg															
190 195 200															
aag aag tgt cag aag gga gaa cga gga aaa aaa gga agg gag agg aaa															915
Lys Lys Cys Gln Lys Gly Glu Arg Gly Lys Lys Gly Arg Glu Arg Lys															
205 210 215															

aga aaa aaa cct aat aaa gga gaa agt aaa gaa gca ata cct gac agc 963  
 Arg Lys Lys Pro Asn Lys Gly Glu Ser Lys Glu Ala Ile Pro Asp Ser  
 220 225 230 235

aaa agt ctg gaa tcc agc aaa gaa atc cca gag caa cga gaa aac aaa 1011  
 Lys Ser Leu Glu Ser Ser Lys Glu Ile Pro Glu Gln Arg Glu Asn Lys  
 240 245 250

cag cag cag aag aag cga aaa gtc caa gat aaa cag aaa tcg gta tca 1059  
 Gln Gln Gln Lys Lys Arg Lys Val Gln Asp Lys Gln Lys Ser Val Ser  
 255 260 265

gtc agc act gta cac tagagggttc catgagatta ttgtagactc atgatgctgc 1114  
 Val Ser Thr Val His  
 270

tatctcaacc agatgcccag gacagggtgct ctagccatta ggaccacaaa tggacatgctc 1174

agttattgct ctgtctaaac aacattccca gtagttgcta tattcttcat acaagcatag 1234

ttaacaacaa agagccaaaa gatcaaagaa gggatacttt cagatgggtg tcttgtgtgc 1294

ttctctgcat ttttaaaaga caagacattc ttgtacatat tatcaatagg ctataagatg 1354

taacaacgaa atgatgacat ctggagaaga aacatctttt ccttataaaa atgtgttttc 1414

aagctgttgt ttttaagaagc aaaagatagt tctgcaaatt caaagataca gtatcccttc 1474

aaaacaaata ggagttcagg gaagagaaac atccttcaaa ggacagtgtt gttttgaccg 1534

ggagatctag agagtgtctca gaattagggc ctggcatttg gaatcacagg atttatcatc 1594

acagaaacaa ctgttttaag attagttcca tcactctcat cctgtatttt tataagaaac 1654

acaagagtgc ataccagaat tgaatatacc atatgggatt ggagaaagac aaatgtggaa 1714

gaaatcatag agctggagac tacttttgtg ctttacaaaa ctgtgaagga ttgtggtcac 1774

ctggaacagg tctccaatct atgttagcac tatgtggctc agcctctgtt accccttgga 1834

ttatatatca acctgtaaac atgtgcctgt aacttacttc caaaaacaaa atcatactta 1894

ttagaagaaa attctgattt tatagaaaaa aaatagagca aggagaatat aacatgtttg 1954

caaagtcatg tgttttcttt ctcaatgagg gaaaaacaat tttattacct gcttaatggg 2014

ccacctggaa ctaaaaggga tactattttc taacaaggta tatctagtag gggagaaagc 2074

caccacaata aatatatttg ttaatag 2101

<210> 34

<211> 272

<212> PRT

<213> Homo sapiens

<400> 34

Met His Leu Arg Leu Ile Ser Trp Leu Phe Ile Ile Leu Asn Phe Met

1

5

10

15

Glu Tyr Ile Gly Ser Gln Asn Ala Ser Arg Gly Arg Arg Gln Arg Arg  
                   20                                  25                                  30  
 Met His Pro Asn Val Ser Gln Gly Cys Gln Gly Gly Cys Ala Thr Cys  
                   35                                  40                                  45  
 Ser Asp Tyr Asn Gly Cys Leu Ser Cys Lys Pro Arg Leu Phe Phe Ala  
                   50                                  55                                  60  
 Leu Glu Arg Ile Gly Met Lys Gln Ile Gly Val Cys Leu Ser Ser Cys  
                   65                                  70                                  75                                  80  
 Pro Ser Gly Tyr Tyr Gly Thr Arg Tyr Pro Asp Ile Asn Lys Cys Thr  
                                   85                                  90                                  95  
 Lys Cys Lys Ala Asp Cys Asp Thr Cys Phe Asn Lys Asn Phe Cys Thr  
                   100                                  105                                  110  
 Lys Cys Lys Ser Gly Phe Tyr Leu His Leu Gly Lys Cys Leu Asp Asn  
                   115                                  120                                  125  
 Cys Pro Glu Gly Leu Glu Ala Asn Asn His Thr Met Glu Cys Val Ser  
                   130                                  135                                  140  
 Ile Val His Cys Glu Val Ser Glu Trp Asn Pro Trp Ser Pro Cys Thr  
                   145                                  150                                  155                                  160  
 Lys Lys Gly Lys Thr Cys Gly Phe Lys Arg Gly Thr Glu Thr Arg Val  
                   165                                  170                                  175  
 Arg Glu Ile Ile Gln His Pro Ser Ala Lys Gly Asn Leu Cys Pro Pro  
                   180                                  185                                  190  
 Thr Asn Glu Thr Arg Lys Cys Thr Val Gln Arg Lys Lys Cys Gln Lys  
                   195                                  200                                  205  
 Gly Glu Arg Gly Lys Lys Gly Arg Glu Arg Lys Arg Lys Lys Pro Asn  
                   210                                  215                                  220  
 Lys Gly Glu Ser Lys Glu Ala Ile Pro Asp Ser Lys Ser Leu Glu Ser  
                   225                                  230                                  235                                  240  
 Ser Lys Glu Ile Pro Glu Gln Arg Glu Asn Lys Gln Gln Gln Lys Lys  
                   245                                  250                                  255  
 Arg Lys Val Gln Asp Lys Gln Lys Ser Val Ser Val Ser Thr Val His  
                   260                                  265                                  270

<210> 35

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

<400> 35

agtacaaaga aagaagtgtt c

21



<210> 36  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR primer

<400> 36  
tgagtctaca gtaacctcgc a 21

<210> 37  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR primer

<400> 37  
taatacgact cactataggg 20

<210> 38  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR primer

<400> 38  
tcgcggcgat gccagccacc ccag 24

<210> 39  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR primer

<400> 39  
agcacgccta tcggatgtga gaggagaagt 30

<210> 40  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR primer

<400> 40  
ctattaacaa atatatttat tgtgggtggct 30

<210> 41

<211> 30  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: PCR primer  
  
 <400> 41  
 tgggtggcttt ctcccctact agatatacct 30  
  
 <210> 42  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: PCR primer  
  
 <400> 42  
 gatatttaggt gacactatag 20  
  
 <210> 43  
 <211> 34  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: PCR primer  
  
 <400> 43  
 ccgctcgagc caccatgcac ttgcgactga tttc 34  
  
 <210> 44  
 <211> 29  
 <212> DNA  
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Met His Pro Asn Val Ser Gln Gly Cys Gln Gly Gly Cys Ala Thr Cys  
 35 40 45

Ser Asp Tyr Asn Gly Cys Leu Ser Cys Lys Pro Arg Leu Phe Phe Ala  
 50 55 60

Leu Glu Arg Ile Gly Met Lys Gln Ile Gly Val Cys Leu Ser Ser Cys  
 65 70 75 80

Pro Ser Gly Tyr Tyr Gly Thr Arg Tyr Pro Asp Ile Asn Lys Cys Thr  
 85 90 95

Lys Cys Lys Ala Asp Cys Asp Thr Cys Phe Asn Lys Asn Phe Cys Thr  
 100 105 110

Lys Cys Lys Ser Gly Phe Tyr Leu His Leu Gly Lys Cys Leu Asp Asn  
 115 120 125

Cys Pro Glu Gly Leu Glu Ala Asn Asn His Thr Met Glu Cys Val Ser  
 130 135 140

Ile Val His Cys Glu Val Ser Glu Trp Asn Pro Trp Ser Pro Cys Thr  
 145 150 155 160

Lys Lys Gly Lys Thr Cys Gly Phe Lys Arg Gly Thr Glu Thr Arg Val  
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Arg Glu Ile Ile Gln His Pro Ser Ala Lys Gly Asn Leu Cys Pro Pro  
 180 185 190

Thr Asn Glu Thr Arg Lys Cys Thr Val Gln Arg Lys Lys Cys Gln Lys  
 195 200 205

Gly Glu Arg Gly Lys Lys Gly Arg Glu Arg Lys Arg Lys Lys Pro Asn  
210 215 220

Lys Gly Glu Ser Lys Glu Ala Ile Pro Asp Ser Lys Ser Leu Glu Ser  
225 230 235 240

Ser Lys Glu Ile Pro Glu Gln Arg Glu Asn Lys Gln Gln Gln Lys Lys  
245 250 255

Arg Lys Val Gln Asp Lys Gln Lys Ser Gly Ile Glu Val Thr Leu Ala  
260 265 270

Glu Gly Leu Thr Ser Val Ser Gln Arg Thr Gln Pro Thr Pro Cys Arg  
275 280 285

Arg Arg Tyr Leu  
290